<u>AMENDMENTS TO THE SPECIFICATION:</u>

Please replace the paragraph that begins on page 1, line 4 with the following amended paragraph:

This application claims priority under 35 U.S.C. §120 to U.S. application no. 09/625,139 filed July 25, 2000, <u>now abandoned,</u> and claims benefit under 35 U.S.C. §119(e) of U.S. provisional patent application no. 60/209,266 filed June 2, 2000, both of which are incorporated by reference herein in their ~~entirety~~ <u>entireties</u>.

Please replace the paragraph that begins on page 13, line 15 with the following amended paragraph:

FIG. 3A-C. Protein microsequencing of the 80 kDa protein. **A.** Analysis of a single tryptic (~~GALHIYHQR~~ <u>GGALHIYHQR</u>) (SEQ ID NO: 6) peptide by tandem- mass spectrometry. All possible b- and y-ion series together with identified b-ion series (red) and y-ion series (blue) are shown. **B.** Collision-induced dissociation (CID) spectrum of this peptide is shown. **C.** Four identified peptides from the α2M receptor <u>(*i.e.*, SGFSLGSDGK (SEQ ID NO: 9), GIALDPAMGK (SEQ ID NO: 10), GGALHIYHQR (SEQ ID NO: 11), and VFFTDYGQIPK (SEQ ID NO: 12))</u>, peptide mass, and sequence are shown.

Please replace the paragraph that begins on page 13, line 29 with the following amended paragraph:

FIG. 6A-B. **A.** The mouse α2MR cDNA (SEQ ID NO: 1) and predicted open reading frame of murine α2MR protein (Genbank accession no. CAA47817). **B.** The murine ~~α2M~~ <u>α2MR</u> protein (SEQ ID NO: 2), with residues identified by microsequencing an 80 kDa, gp96-interacting fragment of the receptor highlighted in bold.

Please replace the paragraph that begins on page 13, line 34 with the following amended paragraph:

FIG. 7A-B. **A.** <u>Translated amino</u> ~~Amino~~ acid sequence of α2M (SEQ ID NO: 3)~~.~~ ~~B. Nucleotide~~ <u>and nucleotide</u> sequence of α2M (SEQ ID NO: 4). **B.** <u>Amino acid sequence of mature α2M (SEQ ID NO.: 8).</u> The 138 amino acid sequence (SEQ ID NO.: 5) of the receptor binding domain from α2M is ~~underlined~~ <u>highlighted</u>.

Please replace the paragraph that begins on page 15, line 7 with the following

amended paragraph:

It is contemplated that the definition of α2M, as used herein, embraces other polypeptide fragments, analogs, and variants of α2M having at least 35% to 55%, preferably 55% to 75%, and most preferably 75% to 85% amino acid identity with α2M, and is capable of forming a complex with an antigenic molecule, which complex is capable of being taken up by an antigen presenting cell and eliciting an immune response against the antigenic molecule. The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al., 1990, J. Mol. Biol. 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, 1997, Nucleic Acids Res.25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Altschul *et al.*, 1997, *supra*). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used ~~(see http://www.ncbi.nlm.nih.gov)~~. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, CABIOS 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Please replace the paragraph that begins on page 16, line 18 with the following amended paragraph:

Amino acid sequences and nucleotide sequences of naturally occurring α2M polypeptides are generally available in sequence databases, such as GenBank. Non-limiting examples of α2M sequences that can be used for preparation of the α2M polypeptides of the

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invention are as follows: Genbank Accession Nos. M11313, P01023, AAA51551; Kan *et al.*, 1985, Proc. Nat. Acad. Sci. 82: 2282-2286. Due to the degeneracy of the genetic code, the term "α2M gene", as used herein, refers not only to the naturally occurring nucleotide sequence but also encompasses all the other degenerate DNA sequences that encode an α2M polypeptide. Computer programs, such as Entrez, can be used to browse the database, and retrieve any amino acid sequence and genetic sequence data of interest by accession number. These databases can also be searched to identify sequences with various degrees of similarities to a query sequence using programs, such as FASTA and BLAST, which rank the similar sequences by alignment scores and statistics. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, 1997, Nucleic Acids Res.25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Altschul *et al.*, 1997, *supra*). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used ~~(see http://www.ncbi.nlm.nih.gov)~~.

Please replace the sequence listing submitted on May 25, 2004 with the substitute sequence listing submitted herewith.